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ANALYSIS TOOLS

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ID   AE014851   standard; genomic DNA; INV; 251762 BP.
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AC   AE014851; AE014188;
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SV   AE014851.1
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DT   08-OCT-2002 (Rel. 73, Created)
DT   13-FEB-2003 (Rel. 74, Last updated, Version 3)
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DE   Plasmodium falciparum 3D7 chromosome 12, section 8 of 9 of the complete
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KW   .
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OS   Plasmodium falciparum 3D7
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RX   MEDLINE; 22255705.
RX   PUBMED; 12368864.
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RA   Carlton J.M., Pain A., Nelson K.E., Bowman S., Paulsen I.T., James K.,
RA   Eisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyes S., Chan M.S.,
RA   Nene V., Shallom S.J., Suh B., Peterson J., Angiuoli S., Pertea M.,
RA   Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B., Martin D.M.,
RA   Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A., McFadden G.I.,
RA   Cummings L.M., Subramanian G.M., Mungall C., Venter J.C., Carucci D.J.,
RA   Hoffman S.L., Newbold C., Davis R.W., Fraser C.M., Barrell B.;
RT   "Genome sequence of the human malaria parasite Plasmodium falciparum";
RL   Nature 419(6906):498-511(2002).
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RN   [2]
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RA   Hyman R.W., Fung E., Conway A., Kurdi O., Mao J., Miranda M., Nakao B.,
RA   Rowley D., Tamaki T., Wang F., Davis R.W.;
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RL   Submitted (13-SEP-2002) to the EMBL/GenBank/DDBJ databases.
RL   Stanford Genome Technology Center, Stanford University, 855 California
RL   Avenue, Palo Alto, CA 94304, USA
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RL   Submitted (29-JAN-2003) to the EMBL/GenBank/DDBJ databases.
RL   Stanford Genome Technology Center, Stanford University, 855 California
RL   Avenue, Palo Alto, CA 94304, USA
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FT                                   /product="hypothetical protein"
FT                                   /locus_tag="PFL1995c"
FT                                   /protein_id="AAN36483.1"
FT                                   /translation="MNKKLEKSFSFIRNFAEKYKNVIFHGFKKGTVKTINKKNRKKKKQ
FT                 NVTNIVDLKFKNPFINEEKKRKLDSFLMDQENELDLHENYTLFNKYNMTSDNLFFNLKN
FT                 DNLYNNNNNTSGTFLKSLNIENKNGDLSDDKIKINYLDSLNSLELKIKQEIKQNNDLL
FT                 SKQKMMELNEYHYKTHNNGKKSEVRIKRTNSHLNKDSNRIYKRRKNNESQLDNVSIKSK
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FT                            16760..16822,16922..16983,17144..>17284)
FT                            /locus_tag="PFL2000w"
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FT                            /note="HMMPfam hit to PF00153, Mitochondrial carrier
FT                            protein, score 3.3e-14"
FT                            /product="mitochondrial carrier protein, putative"
FT                            /locus_tag="PFL2000w"
FT                            /protein_id="AAN36484.1"
FT                            /translation="MEHLKNLITGAISGAIVDAVLFPIDYIKTNIQTNNSFSIYDPRKL
FT                            YNGILPTLIGTVPASAFFYCFYELSKKLLTDYNANINKSSLYLISTSIAEITACIIRLP
FT                            FEILKQNMQVSGNISTLKAIYNISKKNDLPIYLLNSYLIMVAREIPFDCIQYFLWESLK
FT                            EKGKKDFKNISEIYPTLTSALCGGIAGGISGFLTTPVDVIKSRQIIYGKSYIETIKDIS
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FT                   /db_xref="SPTREMBL:Q8I512"
FT                   /note="HMMPfam hit to PF00004, ATPase family associated
FT                   with various cellular activities (AAA), score 1.1e-11"
FT                   /product="replication factor c subunit 4"
FT                   /locus_tag="PFL2005w"
FT                   /protein_id="AAN36485.1"
FT                   /translation="MEEDSFKNRLLKRNIDIWIEKYRPEFLDEVVGNPFVINTLKSIIT
FT                   SGNMPNLLLAGAPGTGKTTSILCLASEMLGNQAKKAVLELNASDDRGINVIRDRIKSFA
FT                   KEIISLPPGKHKIIILDEVDSMTTAAQQSLRRIMELYSDTTRFALACNQSEKIIDALQS
FT                   RCAIIRYFKLSDDQVLKRILKICDLENIKYTDDGLDALTFIADGDLRKAVNCLQSTYAG
FT                   LEVINKENVLHICDIPSPERIENLLKHCVNSEWKKAHDIAYSMIKEGHTPYDISLTSSN
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FT                   /locus_tag="PFL2010c"
FT   CDS             join(complement(20718..23350),complement(20626..20677))
FT                   /codon_start=1
FT                   /db_xref="GOA:Q8I511"
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FT                   /note="HMMPfam hit to PF00270, DEAD/DEAH box helicase,
FT                   score 8.3e-42"
FT                   /product="DEAD/DEAH box helicase, putative"
FT                   /locus_tag="PFL2010c"
FT                   /protein_id="AAN36486.1"
FT                   /translation="MNDAQIKDMMNDEEEKEEIEIKENINDKINEIDDNDDNDDGDDDG
FT                   DDDDEDEDEDSDDNDDEDNDEDEDNDDNDDNDDSDNNDDDHNDVKKSSKNKKKNNEEMF
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FT                          KIIQKNNTNNKNKNNNNNIKPFALKNNNGLVITEQGYESQLTKEPEREVADPSKLPPLC
FT                          GQRLRNYMYLKYIKGKKNKNGSNMNKSYNSNNKKRKNNNKYNNRYNKYNKKGINKNHNK
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FT                              /product="hypothetical protein"
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FT                           KILIEKYLCKNVNFNYNDLRICMNSSYILPEKKNKKKNEIYHFLFGYKNDKNKEEIKDS
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FT                              /note="HMMPfam hit to PF00833, Ribosomal S17, score
FT                              1.8e-63"
FT                              /product="40S ribosomal protein S17, putative"
FT                              /locus_tag="PFL2055w"
FT                              /protein_id="AAN36495.1"
FT                              /translation="MGRVRTKTIKRAARQIVEKYYAKLTLDFQINKKITEEVAIIPSKR
FT                              MKNKVAGFVTHLMKRIQKGPVRGISLKLQEEERERRLDFVPEKSQIDVSVIYVEPDTLR
FT                              MIKSLGINISNMKVHNPMINTNQQKQNRMNNQF"
FT      repeat_region   complement(44363..44413)
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FT                   complement(47436..47528),complement(<46082..47289))
FT                           /locus_tag="PFL2060c"
FT   CDS             join(complement(48041..48058),complement(47715..47775),
FT                   complement(47436..47528),complement(46082..47289))
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FT                           /db_xref="SPTREMBL:Q8I501"
FT                           /note="HMMPfam hit to PF00996, GDP dissociation inhibitor,
FT                   score 0"
FT                           /product="rabGDI protein"
FT                           /locus_tag="PFL2060c"
FT                           /protein_id="AAN36496.1"
FT                           /translation="MNEHYDVIILGTGLKECILSGLLSHYGKKILVLDRNPYYGGETAS
FT                   LNLTNLYNTFKPKENIPSKYGENRHWNVDLIPKFILVGGNLVKILKKTRVTNYLEWLVV
FT                   EGSYVYQHQKKGFLTSEKFIHKVPATDMEALVSPLLSLMEKNRCKNFYQYVSEWDANKR
FT                   NTWDNLDPYKLTMLEIYKHFNLCQLTIDFLGHAVALYLNDDYLKQPAYLTLERIKLYMQ
FT                   SISAFGKSPFIYPLYGLGGIPEGFSRMCAINGGTFMLNKNVVDFVFDDDNKVCGIKSSD
FT                   GEIAYCDKVICDPSYVMHLKNKIKKIGQVIRCICILSNPIPETNQTNSCQIIIPQNQLN
FT                   RKSDIYINLVSFQHGVTLKGKYIAIVSATVETNNPIKEIEKPLELLGTIEEKFVKISDL
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FT                   N"
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FT                           /locus_tag="PFL2065c"
FT      CDS              join(complement(50244..50324),complement(49985..50157),
FT                       complement(49580..49637))
FT                           /codon_start=1
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FT                                  finger, score 5.5e-10"
FT                                  /product="mitochondrial import inner membrane translocase
FT                                  subunit, putative"
FT                                  /locus_tag="PFL2065c"
FT                                  /protein_id="AAN36497.1"
FT                                  /translation="MDLSSLPTDDNLDDKKRAAVCLKKLIYVLLSLQEIVQKQKENVKV
FT                                  MDICFNKCVSKIGPKLSSSEQKCIWDCANSYFYTNVFLNQRLEQMTKILKSNSDYTNL"
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FT                          /note="HMMPfam hit to PF00804, Syntaxin, score 0.0001"
FT                          /product="t-SNARE, putative"
FT                          /locus_tag="PFL2070w"
FT                          /protein_id="AAN36498.1"
FT                          /translation="MEVIYRNITNTYFDYRREIKKKKNRFKLRAYEKLDEDEDTGKENL
FT                          LNENEDLEMQEQSMLPPYWIEKIEECSEDINNMKTKLIQLQKLQKNKLLNALNNDETLT
FT                          ENITQLSSNITFLIKNCEQKIQSVSSKDYDKDKNNIIEKLKNNAKSSLLSQLQSLSQTF
FT                          HKNQKSYIKEFKKMSNAYDDLQQYQNFNEQNELLYQQEEQQHSSVNMNKRNSDLKKIAD
FT                          TVVDLHTIFKELSVMLVDQGSLLDQIDYNMEASLDKSEKGINKLKIIEKRENDKIAKKC
FT                          VSYLTTLIFVLLFLIIIKHLY"
FT   repeat_region   complement(53352..53384)
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FT                              /db_xref="GOA:Q8I4Z8"
FT                              /db_xref="SPTREMBL:Q8I4Z8"
FT                              /note="HMMSmart hit to SM00451, U1-like zinc finger, score
FT                              1.6e-09"
FT                              /product="hypothetical protein, conserved"
FT                              /locus_tag="PFL2075c"
FT                              /protein_id="AAN36499.1"
FT                              /translation="MSKKRKSYENDEDVYDNKRNKKNVASSIDSYGRKVWDKEYYQKKV
FT                              DEKVENDEDELILKLLPDLKKKSKLEPPPPSERKLLEERKENLLLEKNLGKVQILTQKT
FT                              PKNEQGGYYCKICDCVLKDSQTYLDHINGKNHNRMLGYSMKVKKVTLDDVKKRLSLLKD
FT                              KKQNKTEDVEKDPYEDAKKNLKDMQEDEERRIQKRKEKKMLKKLEKEKKKNENENENND
FT                              EESDNMNMMFKEMGLPTSFV"
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FT                              /db_xref="SPTREMBL:Q8I4Z7"
FT                              /product="hypothetical protein"
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FT                          /product="hypothetical protein"
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FT                              5.3e-09, 31.602% id in 231 aa, and to Arabidopsis thaliana
FT                              hypothetical 24.3 kda protein TR:Q9SZE4 (EMBL:AL078470)
FT                              (219 aa) fasta scores: E(): 2.3e-07, 29.384% id in 211 aa"
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FT                   FMTKPSESVIEVLRRKNFLLDDPNNTKTINMSREAFSWFLKDLRSRIISLVLEYLLIID
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